



SEQUENCE LISTING

<110> BATHE, BRIGITTE
KREUTZER, CAROLINE
MARX, ACHIM
PFEFFERLE, WALTER

<120> NEW NUCLEOTIDE SEQUENCES WHICH CODE FOR THE
LUXS GENE

<130> MAS/21123/280106

<140> 09/824,551
<141> 2001-04-04

<160> 4

<170> PatentIn Ver. 2.1

<210> 1
<211> 1902
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (342)..(1610)
<223> luxS-Gen

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cggtgcggtc gaccgcgggc atcgcgtcga tggaaaggcc gtcagtaatt acttccgggg 180
ctgcctcggt ggtggtctct ggggttgctt caggttccgc cggggtaaca gcggtgagca 240
tcatggaaagc agcgaggata gtaggtaatg tacgacgcat gcagtcaagc ctagatcg 300
tgtcggaaac cggacgcaat gagctcgatg ttgaaaccct t qtg aag aag ggg aat 356
Met Lys Lys Gly Asn
1 5

caa ccg ggc gcg atg agc tat cgc aac agt atc cac att ttg aca gcc 404
Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile His Ile Leu Thr Ala
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tgc ctg ctg gtc gtg ggg ttg gga gct tcc gcc cgc ctg acg ctg ccg 452
Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro
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atg ttt gcg ctg tgc gtg ctg ttg ttt gtg tgg ggt ttt ctg tac 500
Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val Trp Gly Phe Leu Tyr
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ttc tat gga tca acc aaa cgc gta gat ttg agc cac ggc atg cag ctg	548
Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser His Gly Met Gln Leu	
55 60 65	
ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att ttt atg gtg ccg atc	596
Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile Phe Met Val Pro Ile	
70 75 80 85	
gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg ttt ttc ctc tat cta	644
Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu	
90 95 100	
cag gtg atg cct gac gtg aga ggc att att gcg att ttg ggt gcg aca	692
Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr	
105 110 115	
gcg att gcg att gcc agc cag tat tcc gtg ggg ttg acc ttt ggt ggt	740
Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly	
120 125 130	
gtg atg ggt ccg gtg gtc tct gcg atc gtg acc gtg gct att gat tac	788
Val Met Gly Pro Val Val Ser Ala Ile Val Thr Val Ala Ile Asp Tyr	
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Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu Lys Gln Glu Leu Ile	
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gat cag ttg att gaa act cgc tcc cag ctg gcg gtg acg gaa cga aat	884
Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala Val Thr Glu Arg Asn	
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gcg ggt att gct gcg gaa cgt caa cgt att gcg cat gaa att cat gac	932
Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala His Glu Ile His Asp	
185 190 195	
acg gtc gcc cag gga ctc tcc tcc att caa atg ctg ctg cat gtc tct	980
Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met Leu Leu His Val Ser	
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gaa cag gag att ctc gtt gct gag atg gaa gag aag cca aag gag gcg	1028
Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu Lys Pro Lys Glu Ala	
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atc gtg aag aag atg cgc ctt gcc cga caa aca gcc tcc gac aat ctc	1076
Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu	
230 235 240 245	
agt gag gct cgc gcg atg att gcg gcg ttg caa ccg gca gcg ctg tct	1124
Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser	
250 255 260	
aaa acc tcc ttg gaa gca gca ctt cac cgc gtc aca gaa ccg ttg ttg	1172
Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val Thr Glu Pro Leu Leu	
265 270 275	

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 atg aaa act gaa gcc acc ctt ctg cga att gct caa ggt gcg atc gga 1268
 Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly
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 Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys His Val Thr Leu Thr
 310 315 320 325
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 Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val Asp Asp Gly Val Gly
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 Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala Gly Leu Gly His Ile
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 Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu Leu His Gly Glu Val
 360 365 370
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 Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala Val Ser Ala Ala Leu
 375 380 385
 ccg gtg gag cca cca gag ggg ttt gtc ggg gcg ccg gtt ttg gca gat 1556
 Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala Pro Val Leu Ala Asp
 390 395 400 405
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 Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu Ser Ser Pro Thr Asp
 410 415 420
 gat gag taaggctaga ctaaagtacg attcatctgc tcatcgatac tcttgaaggc 1660
 Asp Glu
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 <213> *Corynebacterium glutamicum*

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Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val
 35 40 45

Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
 50 55 60

His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
 65 70 75 80

Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
 85 90 95

Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
 100 105 110

Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly
 115 120 125

Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr
 130 135 140

Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu
 145 150 155 160

Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala
 165 170 175

Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala
 180 185 190

His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met
 195 200 205

Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu
 210 215 220

Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr
 225 230 235 240

Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln
 245 250 255

Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
 260 265 270

Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
 275 280 285

Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
 290 295 300

Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
 305 310 315 320

Al
 Cm^{1/2}

His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val
 325 330 335
 Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
 340 345 350
 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
 355 360 365
 Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
 370 375 380
 Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
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*AI
Conclu.*

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 <223> Primer luxS-int1

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